

Using Climate and Genetic Diversity Data to Prioritize Conservation Seed Banking for Imperiled Hemlock Species¹

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Hemlock woolly adelgid (HWA, *Adelges tsugae*) is an invasive forest insect that has caused mortality of eastern (*Tsuga canadensis*) and Carolina hemlock (*T. caroliniana*) at an alarming rate. Now infesting 19 states and over 400 counties of the eastern United States, HWA poses a significant threat to native host species. The current biological and chemical methods for protecting these keystone species are expensive, time consuming, and short-lived. For the long-term preservation of both hemlock species, *ex situ* genetic conservation efforts such as seed collection and storage may be the best solution. With this in mind, it is urgent to prioritize populations within the native range of eastern and Carolina hemlock for *ex situ* conservation. Using a geographic information systems technique called gap analysis in congruence with eight genetic diversity estimates, areas of significant eastern and Carolina hemlock genetic diversity were located and threats to those areas were identified. Using the Multivariate Adaptive Constructed Analogs statistical downscaling method, climate projections averaged over 20 regional climate models were analyzed to display a minimum temperature threshold below which significant HWA mortality occurs. Models also show the temporal northward movement of that threshold to areas not yet exposed to HWA. The result is a spatially weighted index of hemlock populations prioritized by genetic significance and climatic risk. Through 12 years of seed collection and seed banking of eastern and Carolina hemlock, we have also collected the genetic diversity data needed to refine ongoing efforts to prioritize populations most at risk and those that encompass the highest levels of genetic diversity.

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